



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/729,658A

RECEIVED

MAY 21 2001

Source: 1632

TECH CENTER 1600/2900

Date Processed by STIC: 5/4/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/229,658A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE	
1 <input type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
11 <input type="checkbox"/> Use of "Artificial" (NEW RULES)	Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

1632

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658A

DATE: 05/04/2001
TIME: 16:25:41

Input Set : A:\55924.app
Output Set: N:\CRF3\05042001\I729658A raw

3 <110> APPLICANT: Zonana et al.
4 <120> TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
5 <130> FILE REFERENCE: 55924
6 <140> CURRENT APPLICATION NUMBER: 09/729,658A
7 <141> CURRENT FILING DATE: 2000-12-04
8 <150> PRIOR APPLICATION NUMBER: 09/342,681
9 <151> PRIOR FILING DATE: 1999-06-29
10 <150> PRIOR APPLICATION NUMBER: 60/092,279
11 <151> PRIOR FILING DATE: 1998-07-09
12 <150> PRIOR APPLICATION NUMBER: 60/112,366
13 <151> PRIOR FILING DATE: 1998-12-15
14 <160> NUMBER OF SEQ ID NOS: 122
15 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed

roteins

ERRORED SEQUENCES

2619 <210> SEQ ID NO: 3 **093**
2620 <211> LENGTH: 19
2621 <212> TYPE: DNA
2622 <213> ORGANISM: Artificial Sequence
2624 <220> FEATURE:
2625 <223> OTHER INFORMATION: Description of Artificial Sequence:
2626 Oligonucleotide primers that can be used for
2627 mutation screening of human DL.
EK-> 2629 <400> SEQUENCE: 93
2630 ctcgttggat cttggctt
EK-> 2633 <210> SEQ ID NO: 94
2750 <210> SEQ ID NO: 101
2751 <211> LENGTH: 1169
2752 <212> TYPE: DNA
2753 <213> ORGANISM: Homo sapiens
2755 <400> SEQUENCE: 101
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2758 cctggcctt gtccccatccc acaaggagca gcatccagga cgagagatcc tggccctcc 180
2759 ggtggacagg cagcccatca ggctctgcct ctgtgtctcc taagtggcca ttaaccatca 240
2760 taatatctt tgaccaccaa aaggaaacaa attgttggaa tacttagt gcaatgtggcc 300
E--> 2761 atgtgaaaca ctttggaaa aagaaaacifn naattttatn caaaaagcag tatttttatn 360
E--> 2762 attctggnaa cactctggnn aahctactaa taanntanat ntgagaaaaag aaataatn 420
E--> 2763 gangagatta tgannncgaa gnnaagnnan gnanaancan annagntnn agaaaatgag 480
E--> 2764 gttgnnaang antnataana tagnacanng ntgattnca ntggaaagta aacngcntga 540
E--> 2765 gnannagtga ttgtgtatng ccagggtatt ctnngagggaa aacangact aacngcntga 600
E--> 2766 anngtgngga aaggncacaa cngtgnntna ncataganaa nntagatgtt ntgggtggcc 660
E--> 2767 attnnaanna gcnngttaag aatagcttg aagtngncaa ggggtncag aggcaannnt 720
E--> 2768 aatgcctata natccctataa gnntgcagge tantggngan ggtgctnaca aagagcatgt 780
E--> 2769 tcctcttcca ggaaggcttg gccttngttt gtgttnacccc tggggggcta ancaggccnt 840

→ item 10
on Error
summary
sheet

item 10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658A

DATE: 05/04/2001

TIME: 16:25:42

Input Set : A:\55924.app

Output Set: N:\CRF3\05042001\I729658A.raw

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 2771 gccaccagag agaggaacca gaaaggggct gagatcaaaa gaaaggccca cttggcagc 960
 2772 tcaatattgt taaaagaatg ctccatttc agacaggctg aaaccccaag gaaactgagt 1020
 2773 ggacagagca ggtgacttag tggcgctggc ctcatcccc acttgattgt gggcctgcag 1080
 2774 actggccacc gtgtctctg caccagtccc tgcctgtgtg ctgtccagct cacctgtcta 1140
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 2789 <211> LENGTH: 484
 2790 <212> TYPE: DNA
 2791 <213> ORGANISM: Homo sapiens
 2793 <400> SEQUENCE: 103
 2794 gtgaggtgtct ttgtccttcc accagcacgg tatttggta ggcacggatc tctttcacta 60
 2795 cagaggggtt aggaaagagc cgggtcctggc acctggacaa ggtaatcac agtaacagca 120
 2796 ctatgtaaaatg tgctcctgtg gcctgtccag gcagggttat gaagggaggg gcgtttgcca 180
 2797 catctgagcc ttgagtcaga ggctgaggtt ctatgtcagg ttggccacca gtcacctgac 240
 E--> 2798 aagtcaacttta acctccatgt gcctcggtt tctcatcggtt aatatgggg tgaagaaagn 300
 E--> 2799 acaatancga tgactcttta gggttcattt aacagtctaa gaaataaaaaa tatttagctc 360 item 10
 2800 ccctcagcca tcactgcctc aggccccatc atgatcatga atccagatcc atgagctctg 420
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 2802 gcag 484
 2815 <210> SEQ ID NO: 105
 2816 <211> LENGTH: 799
 2817 <212> TYPE: DNA
 2818 <213> ORGANISM: Homo sapiens
 2820 <400> SEQUENCE: 105
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 2822 gaagaggaga gaaatgatc atgatgtatg attatggtc gcttccccac ctggcctcac 120
 2823 ctccctaaatg taatttgcattt acatgttgc cccctgtcag gaagtcattt tatctgcaat 180
 2824 cagatgtatgg ctgtcctggg accgtctggg ggtgctggg gtgaaggcgg 240
 2825 gggcatagcg gcagggtggc agcacaggca gtcgaagcc cggccaggag gagagaccag 300
 E--> 2826 gcgtcctggg ctgttgcagg ggccngagtt aacagcaattt ctatcaactt ttttcatata 360
 E--> 2827 aacatgtca ccatagcaact ttaatattaa ctgtcanaan gtncattttt attctncctt 420
 E--> 2828 aaccaggaa gangggatcg nggaggaccc caangttttt tntgcctctc acanttagnc 480
 E--> 2829 cccacntgg ctgtgnctna aggttgcctt aagcgttgc agcgttgc ggcgagaagca agctccctt 540
 E--> 2830 ggaacaatna ggtanccca gaaaaagtct gganaggcca agtctgaggg cagcggcagc 600 item 10
 E--> 2831 gggttgtggg cagtcctggc ctggcagcca aaaccagcgc gnaggatttg gtttcagtc 660
 2832 taagcaagca cctcagattt cagggttccc tggatcattt ccaggggcag ggcatttgt 720
 2833 tccaggggcc gggatcctgg agggaaagacc agcagggttc ctgatctg ggtcattcat 780
 2834 gccttccttc cacccacag 799
 2868 <210> SEQ ID NO: 109
 2869 <211> LENGTH: 243
 2870 <212> TYPE: DNA
 2871 <213> ORGANISM: Homo sapiens
 2873 <400> SEQUENCE: 109
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 2875 ttcccagaag cagccctctc gtcgttctg ctctcacatg ctgaaccata ctgtgtttac 120
 2876 cgtgggggtgg tgccacacag acaccggca gtcgtccca acaggaagag cagggttggg 180
 E--> 2877 ctgagcgcac agccatgtac caattctaac tcctatctcc ccaacctccc cattttccctg 240 item 10
 2878 cag 243

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658A

DATE: 05/04/2001
TIME: 16:25:42

Input Set : A:\55924.app
Output Set : N:\

Output Set: N:\CRF3\05042001\I729658A.raw

item 10

E--> 2960 agnagtgaga ngggaaaggna nagngagnag gggnnangag aaagngggag ntaggnggc 180 Item 10
E--> 2961 gatgnnnng gtngaaatat tnanagaaat ttttcaaatt aatttttatt tcatttaaat 240
2962 aattttcag ttttgacctt ctattgactg tgacttgcaa catctaactg tggccattgg 300
2963 tgtctgtag 309
2966 <210> SEQ ID NO: 116
2967 <211> LENGTH: 2781
2968 <212> TYPE: DNA
2969 <213> ORGANISM: Homo sapiens
2971 <400> SEQUENCE: 116
2972 gtcttagccc cacggagctg ccatttgatt gcotcgagaa gactagccga atgctcagct 60
2973 ccaacgtacaa ctctgagaag gctgttgta aaacgtggcg ccacccgc gagaggttcg 120
2974 gcctgaagag ggatggatt gggggcatga cagacggcat gcaactctt gaccgcata 180
2975 gcaacggcagg ctacagcatc cttcgactac tcacaaaact ggtgcagatt gagcggctgg 240
2976 atgtgttgc gtccttgcg acagacatac tggagtggc ggggggtgtt ccacccgcct 300
2977 cccagccaca tgctgcattc tgaaaacat gcctgtggc tggctccca ggacaaggca 360
2978 aggatccaac gagggtctg gagctgttag tggccaaa agactgccaa gaatcaaggc 420
2979 ttttgtata tggccatc tgccttaga tggtcaagga gccagacgaa ataaggcctg 480
E--> 2980 tcttccaatt taaccaaaga taaaggacta gagccggat actttcanat gtcgcctgt 540 Item 10
2981 acctcaccag gcagagtaaa tatctactca ctcatacagc cagccacca gcccaccatt 600
E--> 2982 aactcactga acaatgagac aatgtngagg actcaaatga atcaaaccccc 660
E--> 2983 cagantgaag aatctggtc ctgtctttaa ggagtttgca ctccaggtaga agacagaagg 720
2984 aacgtatgtt tacaaaaccac ttcaactggaa gacgtcaaac aagctgaatg aagggggcgt 780
2985 tagaaaacgt taatagaagt tctaagcggg agatgactcc ctactgggat gatgaaggat 840
2986 ggcattccatc tgaagaagca gctcaaacat tttgtaaaaa tggcaacaaa atgcagacac 900
2987 cctgtccatc gtattatttc aggttttaga caagtcgtt aataccctat gtggtttcat 960
2988 taggataact ttttacctat ctttgaggc atccatattt ttacaggcct tccaggtaat 1020
2989 aatgaaagag ctcactctat acaaaaaccaa tatgaaggc atgtgtttgtt ccaagcaatt 1080
2990 ggatgtgtgc agtagccat ttcatattact gcattactt tggccttggg aaccctgtgg 1140
2991 tctgcaactc atgtgaatgg ctttccactt caagtccttgc gcaaggatgg ctttttaggg 1200
2992 gcagaatgc tgaaggacac agcaatttaa attataatgt gtcaaggctgt gttttcactt 1260
2993 caaacatgtc tgtagtagtca gctgttaattt gagaatgt gacttcattt gagttcagcc 1320
2994 acgcataatt cttagatttca agagcatota agacttgcattt attagcctca tggcatgaga 1380
2995 gtttcagact cggcttcgt agccagtcg ggaaagtgg gtttcgcgc gcaaatgaga 1440
2996 gcctggcctt ggtgtcgagg gagctggctt ctgtgtgc caccattggc cttgtcttt 1500
2997 cctctctctg ctcctgttcc tgcgtgcata atgagatgtt agttgtat tctataattt 1560
2998 gggcaggtag ggttcagggt agcaaaaaga aagtggagct ataggaaatg ccaggcctt 1620
2999 gaggtgcctc atgaaagtca acacagtgtt gtttgcatt ttaatggg ataaaaacac 1680
3000 aaaaactcg acttggcatt ttcaataaa ctgcaatggt ttgacataac atttataggc 1740
3001 agaaagttaa taaactggca ttgttcttgg catattattt tactatccct gtaactgc 1800
3002 agagctcagg agcaggctc gtatcacac caggggttag agttcactgc tgaactccct 1860
3003 gatggcagggt ctgttttactacatca aaacaaatgc tctgactttaa aagcggagg 1920
3004 cgtaaaaattt acaagtgc ttagtggaaa aatgttttag gggaaaatc agtcatatc 1980
3005 ttaacaccaa caagcaattt cccaccaacg aatgttagtac atactgttagg aggatcatata 2040
3006 tgaggctctg aatatttaat atcatcattt actgtgtctg tttgtgtctg tttttcgaaac 2100
E--> 3007 ctatgggtt taccctgcaaa gctaaatactt ccacggcaga ncttaattat ctttttaatt 2160 Item 10
3008 cctcttgaa atcctgtggt gcccccttc cctgccttg tgatgtat gaggatgtct 2220
3009 ccccttaattt agactgcaaa tggccatc tggatgtgtt gatgtgttgc ctttccagg ataaacagctt 2280
3010 gcaccctctt cagaatgttt tggccatc tggccatc tggatgtgttgc ctttccagg tggccatc 2340
3011 tttggccatc tttcacaacta ttggccatc tggccatc tggccatc tggccatc tggccatc 2400

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/729,658A

DATE: 05/04/2001

TIME: 16:25:42

Input Set : A:\55924.app

Output Set: N:\CRF3\05042001\I729658A.raw

3012 tggccattt gctctccacc tgccatTTT agggagctat tccttatata gttacaaatt 2460
 3013 cccttgcat ttacttattt ggaaacatgg gatttactct gacaagctt agcctatgtt 2520
 3014 atgggattca gaacaatgg atcataataa ttctcaactga ccaaagctgg gactccatcc 2580
 3015 tgccatTTT gtgtggatg attcataatt ctgcaatact taaaacatt tagaaaacac 2640
 E--> 3016 cccaggtag gtctgtggcc ottanacagt gaaagtctta attggcaata ttatTTTgc 2700 *new 10*
 E--> 3017 taattctgga tatataaac nnattatatt tataaatctc aataaACCCC atttantaaa 2760
 3018 aaaaaaaaaaaaaaaa aaaaaaaaaaaa a
 3091 <210> SEQ ID NO: 122
 3092 <211> LENGTH: 21
 3093 <212> TYPE: DNA
 3094 <213> ORGANISM: Artificial Sequence
 3096 <220> FEATURE:
 3097 <223> OTHER INFORMATION: Description of Artificial Sequence:
 3098 Oligonucleotide primer that can be used to amplify
 3099 TNF homology domain of mouse dl.
 3101 <400> SEQUENCE: 122
 3102 aagcttcttag gatgcagggg c

21

E--> 3103 1
 E--> 3106 55*delete at end of file**PJS*Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/729,658A

DATE: 05/04/2001

TIME: 16:25:43

Input Set : A:\55924.app

Output Set: N:\CRF3\05042001\I729658A.raw

L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
 L:503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
 L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
 L:742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
 L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
 L:764 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
 L:1930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
 L:2629 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:93
 L:2633 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 4 thru 93
 L:2662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95
 L:2663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95
 L:2664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95
 L:2667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95
 L:2698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95
 L:2699 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97
 L:2700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97
 L:2761 M:340 E: (46) "n" or "Xaa" used, for SEQ ID#:97
 M:340 Repeated in SeqNo=101
 L:2798 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:101
 M:340 Repeated in SeqNo=103
 L:2826 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:103
 M:340 Repeated in SeqNo=105
 L:2877 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:105
 L:2898 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:109
 M:340 Repeated in SeqNo=111
 L:2925 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:112
 L:2939 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:113
 L:2958 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:115
 M:340 Repeated in SeqNo=115
 L:2980 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:116
 M:340 Repeated in SeqNo=116
 L:3103 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:21 SEQ:122
 M:254 Repeated in SeqNo=122